

#2

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/828,607

DATE: 04/23/2001
TIME: 13:23:01

Input Set : A:\Stk070.app
Output Set: N:\CRF3\04232001\I828607.raw

3 <110> APPLICANT: STRYKER CORPORATION
5 <120> TITLE OF INVENTION: REPAIR OF LARYNX, TRACHEA, AND OTHER FIBROCARTILAGINOUS
6 TISSUES
8 <130> FILE REFERENCE: STK-070 PCT
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/828,607
C--> 11 <141> CURRENT FILING DATE: 2001-04-06
13 <160> NUMBER OF SEQ ID NOS: 9
15 <170> SOFTWARE: PatentIn Ver. 2.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1822
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (49)..(1341)
26 <400> SEQUENCE: 1
27 ggtgcgggcc cgagcccg agccggta gcgcgttagag ccggcgcg atg cac gtg 57
28 Met His Val
29 1
31 cgc tca ctg cga gct gct gct gct gct cac agc ttc gtg gct ctc tgg gca 105
32 Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
33 5 10 15
35 ccc ctg ttc ctg ctg cgc tcc gcc ctg gcc gac ttc agc ctg gac aac 153
36 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
37 20 25 30 35
39 gag gtg cac tcg agc ttc atc cac cgg cgc ctc cgc agc cag gag cgg 201
40 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
41 40 45 50
43 cgg gag atg cag cgc gag atc ctc tcc att ttg ggc ttg ccc cac cgc 249
44 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
45 55 60 65
47 ccg cgc ccc cac ctc cag ggc aag cac aac tcg gca ccc atg ttc atg 297
48 Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
49 70 75 80
51 ctg gac ctg tac aac gcc atg gct gtg gag gag ggc ggc ggg ccc ggc 345
52 Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Pro Gly
53 85 90 95
55 ggc cag ggc ttc tcc tac ccc tac aag gcc gtc ttc agt acc cag ggc 393
56 Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
57 100 105 110 115
59 ccc cct ctg gcc agc ctg caa gat agc cat ttc ctc acc gac gcc gac 441
60 Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp
61 120 125 130
63 atg gtc atg agc ttc gtc aac ctc gtg gaa cat gac aag gaa ttc ttc 489
64 Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe
65 135 140 145
67 cac cca cgc tac cac cat cga gag ttc cgg ttt gat ctt tcc aag atc 537

ENTERED

See p.5

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68	His	Pro	Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	Ser	Lys	Ile			
69	150				155				160										
71	cca	gaa	ggg	gaa	gct	gtc	acg	gca	gcc	gaa	ttc	cg	atc	tac	aag	gac	585		
72	Pro	Glu	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Asp			
73	165				170				175										
75	tac	atc	cg	gaa	cgc	ttc	gac	aat	gag	acg	ttc	cg	atc	agc	gtt	tat	633		
76	Tyr	Ile	Arg	Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Arg	Ile	Ser	Val	Tyr			
77	180				185				190				195						
79	cag	gt	ctc	cag	gag	cac	ttg	ggc	agg	gaa	tcg	gat	ctc	ttc	ctg	ctc	681		
80	Gln	Val	Leu	Gln	Glu	His	Leu	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu			
81	200				205				210										
83	gac	agc	cgt	acc	ctc	tgg	gcc	tcg	gag	ggc	tgg	ctg	gtg	ttt	gac		729		
84	Asp	Ser	Arg	Thr	Leu	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe	Asp			
85	215				220				225										
87	atc	aca	gcc	acc	agc	aac	cac	tgg	gt	gtc	aat	ccg	cg	cac	aac	ctg	777		
88	Ile	Thr	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His	Asn	Leu			
89	230				235				240										
91	ggc	ctg	cag	ctc	tcg	gt	gag	acg	ctg	gat	ggg	cag	agc	atc	aac	ccc	825		
92	Gly	Leu	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile	Asn	Pro			
93	245				250				255										
95	aag	ttg	g	gc	ggc	ctg	att	ggg	cg	cc	gg	cc	cag	aac	aag	cg	ccc	873	
96	Lys	Leu	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys	Gln	Pro			
97	260				265				270				275						
99	ttc	atg	gt	gt	gct	ttc	aag	gcc	acg	gag	gtc	cac	ttc	cg	acg	atc	921		
100	Phe	Met	Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Phe	Arg	Ser	Ile			
101	280				285				290										
103	cgg	tcc	acg	ggg	agc	aaa	cag	cgc	acg	aac	cgc	tcc	aag	acg	ccc		969		
104	Arg	Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys	Thr	Pro			
105	295				300				305										
107	aag	aac	cag	gaa	gcc	ctg	cg	atg	gcc	aac	gt	gca	gag	aac	agc	agc	1017		
108	Lys	Asn	Gln	Glu	Ala	Leu	Arg	Met	Ala	Asn	Val	Ala	Glu	Asn	Ser	Ser			
109	310				315				320										
111	agc	gac	cag	agg	cag	gcc	tgt	aag	aag	cac	gag	ctg	tat	gtc	agc	ttc	1065		
112	Ser	Asp	Gln	Arg	Gln	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe			
113	325				330				335										
115	cga	gac	ctg	ggc	tgg	cag	gac	tgg	atc	atc	g	c	c	t	gaa	ggc	tac	gcc	1113
116	Arg	Asp	Leu	Gly	Trp	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala			
117	340				345				350				355						
119	gcc	tac	tac	tgt	gag	ggg	gag	tgt	gcc	ttc	cct	ctg	aac	tcc	tac	atg	1161		
120	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asn	Ser	Tyr	Met			
121	360				365				370										
123	aac	gcc	acc	aac	cac	gcc	atc	gt	g	ac	gt	ctg	gtc	cac	ttc	atc	aac	1209	
124	Asn	Ala	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	His	Phe	Ile	Asn			
125	375				380				385										
127	ccg	gaa	acg	gt	ccc	aag	ccc	tgc	tgt	g	cc	ac	g	at	ctg	aat	gcc	1257	
128	Pro	Glu	Thr	Val	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln	Leu	Asn	Ala			
129	390				395				400										
131	atc	tcc	gtc	ctc	tac	ttc	gat	gac	agc	tcc	aac	gtc	atc	ctg	aag	aaa	1305		
132	Ile	Ser	Val	Leu	Tyr	Phe	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys				

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133	405	410	415	
135	tac aga aac atg gtg gtc cgg gcc tgt ggc tgc cac	tagtcctcc		1351
136	Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His			
137	420	425	430	
139	gagaatttcag acccttggg gccaagttt tctggatcct ccattgctcg ccttggccag	1411		
141	gaaccagcag accaactgcc tttgtgaga cttccccc cctatcccc aactttaaagg	1471		
143	tgtgagagta ttaggaaaca tgagcagcat atggctttg atcagtttt cagtgccagc	1531		
145	atccaatgaa caagatccta caagctgtgc aggcaaaacc tagcagggaaa aaaaaacaac	1591		
147	gcataaaagaa aatggccgg gccaggtcat tggctggaa gtctcagcca tgcacggact	1651		
149	cgtttccaga ggttaattatg aggcctacc agccaggcca cccagccgtg ggaggaaggg	1711		
151	ggcgtggcaa ggggtggca cattgggtc tgtgcgaaag gaaaattgac ccggaagtcc	1771		
153	ctgtataaaa tgtcacaata aaacgaatga atgaaaaaaaaaaaaaaa a	1822		
156	<210> SEQ ID NO: 2			
157	<211> LENGTH: 431			
158	<212> TYPE: PRT			
159	<213> ORGANISM: Homo sapiens			
161	<400> SEQUENCE: 2			
162	Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala			
163	1	5	10	15
165	Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser			
166	20	25	30	
168	Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser			
169	35	40	45	
171	Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu			
172	50	55	60	
174	Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro			
175	65	70	75	80
177	Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly			
178	85	90	95	
180	Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser			
181	100	105	110	
183	Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr			
184	115	120	125	
186	Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys			
187	130	135	140	
189	Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu			
190	145	150	155	160
192	Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile			
193	165	170	175	
195	Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile			
196	180	185	190	
198	Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu			
199	195	200	205	
201	Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu			
202	210	215	220	
204	Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg			
205	225	230	235	240
207	His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser			
208	245	250	255	

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210 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
 211 260 265 270
 213 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
 214 275 280 285
 216 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
 217 290 295 300
 219 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
 220 305 310 315 320
 222 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
 223 325 330 335
 225 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
 226 340 345 350
 228 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
 229 355 360 365
 231 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
 232 370 375 380
 234 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
 235 385 390 395 400
 237 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
 238 405 410 415
 240 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 241 420 425 430
 245 <210> SEQ ID NO: 3
 246 <211> LENGTH: 102
 247 <212> TYPE: PRT
 248 <213> ORGANISM: Artificial Sequence
 250 <220> FEATURE:
 251 <223> OTHER INFORMATION: Description of Artificial Sequence: OPX
 253 <220> FEATURE:
 254 <223> OTHER INFORMATION: each Xaa is independently selected from a group of one
 255 or more specified amino acids as defined in the
 256 specification.
 258 <400> SEQUENCE: 3
 W--> 259 Cys Xaa Xaa His Glu Leu Tyr Val Ser Phe Xaa Asp Leu Gly Trp Xaa
 260 1 5 10 15
 W--> 262 Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
 263 20 25 30
 W--> 265 Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
 266 35 40 45
 W--> 268 Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
 269 50 55 60
 W--> 271 Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
 272 65 70 75 80
 W--> 274 Asp Xaa Ser Xaa Asn Val Ile Leu Xaa Lys Xaa Arg Asn Met Val Val
 275 85 90 95
 W--> 277 Xaa Ala Cys Gly Cys His
 278 100
 281 <210> SEQ ID NO: 4
 282 <211> LENGTH: 97

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Input Set : A:\Stk070.app
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283 <212> TYPE: PRT
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: Description of Artificial Sequence: Generic-Seq-7
289 <220> FEATURE:
290 <223> OTHER INFORMATION: each Xaa is independently selected from a group of one
291 or more specified amino acids as defined in the
292 specification.
294 <400> SEQUENCE: 4
W--> 295 Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa Xaa Xaa Xaa Xaa Xaa
296 1 5 10 15
W--> 298 Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Pro
299 20 25 30
W--> 301 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala Xaa Xaa Xaa Xaa Xaa Xaa
302 35 40 45
W--> 304 Xaa Cys Cys Xaa Pro
305 50 55 60
W--> 307 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
308 65 70 75 80
W--> 310 Val Xaa Leu Xaa Xaa Xaa Xaa Met Xaa Val Xaa Xaa Cys Xaa Cys
311 85 90 95
W--> 313 Xaa
317 <210> SEQ ID NO: 5
318 <211> LENGTH: 102
319 <212> TYPE: PRT
320 <213> ORGANISM: Artificial Sequence
322 <220> FEATURE:
323 <223> OTHER INFORMATION: Description of Artificial Sequence: Generic-Seq-8
325 <220> FEATURE:
326 <223> OTHER INFORMATION: each Xaa is independently selected from a group of one
327 or more specified amino acids as defined in the
328 specification.
330 <400> SEQUENCE: 5
W--> 331 Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa
332 1 5 10 15
W--> 334 Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly
335 20 25 30
W--> 337 Xaa Cys Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala
338 35 40 45
W--> 340 Xaa
341 50 55 60
W--> 343 Xaa Cys Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa
344 65 70 75 80
W--> 346 Xaa Xaa Xaa Xaa Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa Val
347 85 90 95
W--> 349 Xaa Xaa Cys Xaa Cys Xaa
350 100
353 <210> SEQ ID NO: 6
354 <211> LENGTH: 97

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
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Input Set : A:\Stk070.app
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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:259 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:259 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:262 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:262 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:265 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:265 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:265 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:268 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:268 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:271 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:271 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:274 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:274 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:277 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:277 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:295 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:295 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:298 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:298 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:301 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:301 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:304 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:304 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:307 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:307 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:310 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:310 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:313 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:313 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:331 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:331 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:331 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:334 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5

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L:334 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:337 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:337 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:337 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:340 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:340 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:343 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:343 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:346 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:346 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:349 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:349 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:367 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:367 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:370 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:370 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:373 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:373 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:376 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:376 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:382 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:415 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:421 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:439 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9